0590

#2 OIPE

RAW SEQUENCE LISTING DATE: 01/16/2002 PATENT APPLICATION: US/09/955,909 TIME: 11:05:49

Input Set : N:\Crf3\RULE60\09955909.raw
Output Set: N:\CRF3\01162002\1955909.raw

## SEQUENCE LISTING

```
3 (1) GENERAL INFORMATION:
             (i) APPLICANT: PELLETIER, Marc
     5
                            BARKER, William A.
     6
                            HAKES, David J.
     7
                            ZOPF, David A.
     8
            (ii) TITLE OF INVENTION: METHODS FOR PRODUCING
    10
                                     SIALYLOLIGOSACCHARIDES IN A DAIRY SOURCE
    11
           (iii) NUMBER OF SEQUENCES: 10
    13
            (iv) CORRESPONDENCE ADDRESS:
    15
                  (A) ADDRESSEE: PENNIE & EDMONDS LLP
    16
                  (B) STREET: 1155 Avenue of the Americas
    17
                                                             ENTERED
                  (C) CITY: New York
     18
                  (D) STATE: NY
     19
                  (E) COUNTRY: USA
     20
                  (F) ZIP: 10036-2711
     21
             (V) COMPUTER READABLE FORM:
     23
                  (A) MEDIUM TYPE: Diskette
     24
                  (B) COMPUTER: IBM Compatible
     25
                  (C) OPERATING SYSTEM: DOS
     26
                  (D) SOFTWARE: FastSEQ Version 2.0
     27
            (vi) CURRENT APPLICATION DATA:
     29
                  (A) APPLICATION NUMBER: US/09/955,909
C--> 30
                  (B) FILING DATE: 18-Sep-2001
C-->31
                  (C) CLASSIFICATION:
     32
           (vii) PRIOR APPLICATION DATA:
     34
                  (A) APPLICATION NUMBER: 08/911,393
     35
                  (B) FILING DATE:
     36
          (viii) ATTORNEY/AGENT INFORMATION:
     38
                  (A) NAME: Coruzzi, Laura A
     39
                  (B) REGISTRATION NUMBER: 30,742
     40
                  (C) REFERENCE/DOCKET NUMBER: 7188-032-999
     41
            (ix) TELECOMMUNICATION INFORMATION:
     43
                  (A) TELEPHONE: (212)7909090
     44
                  (B) TELEFAX: (212)8699741
     45
                  (C) TELEX: 66141 PENNIE
     46
       (2) INFORMATION FOR SEQ ID NO: 1:
     49
             (i) SEQUENCE CHARACTERISTICS:
     51
                   (A) LENGTH: 3183 base pairs
     52
                   (B) TYPE: nucleic acid
     53
                   (C) STRANDEDNESS: single
     54
                   (D) TOPOLOGY: linear
     55
            (ii) MOLECULE TYPE: cDNA
     57
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     59
         ATGGGGAAAA CAGTCGTTGG GGCCAGTAGG ATGTTCTGGC TAATGTTTTT CGTGCCGCTT
                                                                                 60
         CTTCTTGCGC TCTGCCCCAG CGAGCCCGCG CATGCCCTGG CACCCGGATC GAGCCGAGTT
                                                                                120
     62
         GAGCTGTTTA AGCGGCAAAG CTCGAAGGTG CCATTTGAAA AGGGCGGCAA AGTCACCGAG
                                                                                180
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		ACTCGTTCCG	COMOCOCOCO	CTTCTTAATC	TGGACGGGGT	GATGGTTGCC	240
64	CGGGTTGTCC	CTCGCTACGA	A A CA TICCA A TI	CACAACTCCC	TCATTGATAC	GGTGGCGAAG	300
65	ATCGCGGACG	ACGATGGGGA	CACCTCCCAC	ACCCADATTG	CCATCAAGAA	CAGTCGTGCA	360
66	TACAGCGTGG	ACGATGGGGA CTCGTGTGGT	GACGTGGGAG	CTCATTCTCA	AGGGCAACAA	GCTTTACGTC	420
67	TCGTCTGTTT	CTCGTGTGGT	GGATCCCACA	TACTCGACGT	CGCATGGTGA	TGCGAGAGAC	480
68	CTGGTTGGAA	GCTACAACAG	TTCGAGGAGC	ACCA ACTCCA	CTCCGGGGGG	CAAGATAACT	540
69	TGGGATATTC	TGCTTGCCGT	TGGTGAGGTC	ACGAAGICCA CECAACCAAE	TTTTCCCGGC	GGAAATGGAA	600
70	GCGAGTATCA	AATGGGGGAG	CCCCGTGTCA	CTGAAGGAAI	CCATTGTGGC	GTCCAACGGG	660
71	GGAATGCACA	CAAATCAATT	TCTTGGCGGT	GCAGGIGIIG	AACTTTTTTTC	CAAGATCTTC	720
72	AATCTTGTGT	ACCCTGTGCA	GGTTACGAAC	MANAGAAGC	CTACCACTCA	TTTTGGCTGC	780
73	TACTCGGAAG	ACGAGGGCAA	GACGTGGAAG	TTTGGGGAGG	TANACACTCG	ACTTGACTAT	840
74	TCTGAACCTG	TGGCCCTTGA	GTGGGAGGGG	AAGCTCATCA	CCTCCCTCGA	GGCTGTCGGC	900
75	CGCCGCCGTC	TGGTGTACGA	GTCCAGTGAC	ATGGGGAATT	AGGGGGGGAC	TCACAGCAGC	960
76	ACGCTCTCAC	GTGTGTGGGG	CCCCTCACCA	AAATCGAACC	MGCCCGGCAG	CCTC A A TTTTT	1020
77	TTCACTGCCG	TGACCATCGA	GGGAATGCGT	GTTATGCTCT	TCACACACCC	CCCCATTAT	1080
78	AAGGGAAGGT	GGCTGCGCGA	CCGACTGAAC	CTCTGGCTGA	CGGATAACCA	CCTCTACAAC	1140
79	AACGTTGGGC	AAGTATCCAT	TGGTGATGAA	AATTCCGCCT	ACAGCTCCGT	CCIGIACAAG	1200
80	GATGATAAGC	TGTACTGTTT	GCATGAGATC	AACAGTAACG	AGGTGTACAG	CCTTGTTTT	1260
81	GCGCGCCTGG	TTGGCGAGCT	ACGGATCATT	AAATCAGTGC	TGCAGTCCTG	GAAGAATTGG	1320
82	GACAGCCACC	TGTCCAGCAT	TTGCACCCCT	GCTGATCCAG	CCGCTTCGTC	GTCAGAGCGT	1320
83	CCMMCMCCTC	CCGCTGTCAC	CACGGTTGGT	CTTGTTGGCT	TTTTGTCGCA	CAGTGCCACC	1440
84	$\lambda$ $\lambda$ $\lambda$ $\lambda$ $C$ $C$ $C$ $\Delta$ $\Delta$ $T$	GGGAGGATGC	GTACCGCTGC	GTCAACGCAA	GCACGGCAAA	TGCGGAGAGG	1500
85	CHITCCCAACC	CTTTGAAGTT	TGCGGGGGTT	GGCGGAGGGG	CGCTTTGGCC	GGTGAGCCAG	1560
86	CACCCCCACA	ATCAACGGTA	TCACTTTGCA	AACCACGCGT	TCACGCTGGT	GGCGTCGGTG	1620
87	$\lambda CC\lambda TTC\lambda CC$	AGGTTCCGAG	CGTCGCGAGT	CCTTTGCTGG	GTGCGAGCCT	GGACICITCI	
88	$CCTTCCC\Lambda\Lambda\Lambda\Lambda$	A A CTCCTGGG	GCTCTCGTAC	GACGAGAAGC	: ACCAGTGGCA	GCCAATATAC	1680
89	CCATCAACCC	CGGTGACGCC	GACCGGATCG	TGGGAGATGG	GTAAGAGGTA	CCACGIGGII	1740
90	CTTACCATCC	. ССААТААААТ	TGGTTCGGTG	TACATTGATG	GAGAACCTCT	GGAGGGTTCA	1800
91	CCCCACACCC	TTGTGCCAGA	CGGGAGGACG	CCTGACATCI	CCCACTTCTA	CGTTGGCGGG	1860
92	TATCCAAGCA	GTGATATGCC	: AACCATAAGO	CACGTGACGG	TGAATAATGI	TCTTCTTTAC	1920
93	A A CCCTTCA CC	TCAATGCCGA	GGAGATCAGG	; ACCTTGTTCI	TGAGCCAGG	CCTGATTGGC	1980
94	ACCCAACCAC	ACATGGGCAG	CAGCAGCGG	AGCAGTGCCC	ACAGTACGCC	CTCAACTCCC	2040
95	CCTCACAACC	GTGCCCACAC	TACGCCCTCA	ACTCCCGCTG	ACAGCAGTGC	CCACAGIACG	2100
96	CCCTCA A CTC	CCGCTGACAC	CAGTGCCCAC	AGTACGCCCI	CAGCTCCCGG	TGACAACGGT	2160
97	CCCCACACT	CGCCCTCGAC	TCCCGGTGAC	AGCAGTGCCC	CACAGTACGCC	CTCAACTCCC	2220
98	CCTCACAACC	CTGCCCACAC	TACGCCCTCA	A GCTCCCGCTC	ACAGCAATGO	CCACAGTACG	2280
99	CCCTCCACTC	CCCCTGACA	CGGTGCCCAC	AGTACGCCC	CAACTCCCGC	TGACAACGGT	2340
100	CCCCACAC	PA CGCCCTCGA	AC TCCCGGTG	AC AACGGTGC	CC ACAGTACGO	CTCGACTCCC	2400
100	CCTCACAG	TA GTGCCCACA	G TACGCCCTC	CA ACTCCCGC	rg ACAACGGTC	C CCACAGTACG	2460
103		na accomence	\	AC AGTACGCCC	T CGACTCCC	JG IGACAACGGI	2520
102	CCCCACAC	ra CCCCCTCAC	C TCCCGCTG	AC AGCAATGC	CC ACAGTACGO	CTCGACTCCC	2580
	A COMONONCO	TA GTGCCCAC	AG TACGCCCT	CA GCTCCCGG	rg ACAACGGT	JC CCACAGIACG	2640
104 101	CCCTCACC	PC CCCCTGAC	AG CAGTGCCC	AC AGTACGCC	OT CAGCTCCCC	G TGACAACGGI	2700
	CCCCACACAC	$r_{A}$ $CCCCCTCAC$	C TCCCGCTG	AC AACGGTGC	CC ACAGTACG	CTCAGCICCC	2760
10 10	7 CCTCACACAC	TA ATCCCCAC	AG TACGCCCT	CG ACTCCCGC	IG ACAGCAGT	CCACAGIACG	2820
	ס מממשפא אמי	TO COGOTGAC	AG CAGTGCCC	AC AGTACGCC	CT CAGCTCCC	G TGACAACGGI	2880
10	O CCCCACAC	TA CCCCCTCA	C TCCCGCTG	AC AGCAGTGC	CC ACAGTACG	CTCAATTCCC	2940
10	0	CA GTGCCCAC	AG TACGCCCT	CA GCTCCCGC'	IG ACAGCAGI	3C CCACAGTACG	3000
11	1 CCCTCACC	TO COGGTGAC	AA CGGTGCCC	AC AGTACGCC	CT CGACTCCC	GC TGACAACGGC	3060
11	T CCCICAGC	TO CCCGTORC	AT TTTGCACG	AT GGCGCTGC	AT TTTCGGCC	TT TTCGGGCGGA	3120
11	Z GCIAAIGG	In Courtino		•			

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DATE: 01/16/2002

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Input Set : N:\Crf3\RULE60\09955909.raw Output Set: N:\CRF3\01162002\1955909.raw

113   GGGCTTCTTT TGTGTGCGGG TGCTTTGCTG CTGCACGTGT TCGTTATGGC AGTTTTTTC   3180   114   TGA   3183   116   (2) INFORMATION FOR SEQ ID NO: 2:										~- ~~	mam	maam	നമനം	CC 1	commo	mmmmC	3180
114 TOA  116 (2) INFORMATION FOR SEQ ID NO: 2:  118 (i) SEQUENCE CHARACTERISTICS:  119 (A) LENGTH: 1060 amino acids  120 (B) TYPE: amino acid  121 (C) STRANDEDNESS: Single  122 (D) TOPOLOGY: linear  124 (ii) MOLECULE TYPE: protein  126 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  127 Met Gly Lys Thr Val Val Gly Ala Ser Arg Met Phe Trp Leu Met Phe  129 1 5 10  140 15 15  150 Phe Val Pro Leu Leu Leu Ala Leu Cys Pro Ser Glu Pro Ala His Ala  131 20  132 Leu Ala Pro Gly Ser Ser Arg Val Glu Leu Phe Lys Arg Gln Ser Ser  133 35  140 Lys Val Pro Phe Glu Lys Gly Gly Lys Val Thr Glu Arg Val Val His  155 50  166 Ser Phe Arg Leu Pro Ala Leu Val Asn Val Asp Gly Val Met Val Ala  137 65  138 Ile Ala Asp Ala Arg Tyr Glu Thr Ser Asn Asp Asn Ser Leu Ile Asp  139 90  140 Thr Val Ala Lys Tyr Ser Val Asp Asp Gly Glu Thr Trp Glu Thr Gln  141 100  105 110  142 Ile Ala Ile Lys Asn Ser Arg Ala Ser Ser Val Ser Arg Val Val Asp  143 115  144 Pro Thr Val Ile Val Lys Gly Asn Lys Leu Tyr Val Leu Val Asp  146 Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp  147 145 150  150 Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Arg Ala Gly  151 160  152 Glu Phe Phe Pro Ala Glu Met Glu Gly Met His Thr Asn Gln Phe Leu  155 100  156 Pro Val Gln Val Thr Asn Lys Lys Lys Gly Sen Asn Gly Asn Leu Val Tyr  157 225  158 Cly Lys Fle Thr Ala Ser Ile Lys Trp Lys Phe Gly Glu Gly Arg Ser  159 245  150 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Clu Glu Gly Arg Ser  150 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Clu Glu Gly Arg Ser  157 225  158 Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  159 246  160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Ala Val Tyr Clu  161 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser  164 Ser Asp Met Gly Asn Ser Trp Val Glu Val Val Val Tyr Glu Glu Gly Arg  165 200  179 205  180 300	GGGC	TTCT	TT T	GTGT	GCGG	G TG	CTTT	GCTG	CTG	CACG	TGT	TCGT	TATG	GC A	GITI	11110	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1060 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (Ai) MOLECULE TYPE: protein (Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  Met Gly Lys Thr Val Val Gly Ala Ser Arg Met Phe Trp Leu Met Phe 129 1 5 10 15 130 Phe Val Pro Leu Leu Leu Ala Leu Cys Pro Ser Glu Pro Ala His Ala 131 20 25 132 Leu Ala Pro Gly Ser Ser Arg Val Glu Leu Phe Lys Arg Gln Ser Ser 133 35 134 Lys Val Pro Phe Glu Lys Gly Gly Lys Val Thr Glu Arg Val Val His 135 50 55 136 Ser Phe Arg Leu Pro Ala Leu Val Asn Val Asp Gly Val Met Val Ala 137 65 138 Ile Ala Asp Ala Arg Tyr Glu Thr Ser Asn Asp Asn Ser Leu Ile Asp 139 85 140 Thr Val Ala Lys Tyr Ser Val Asp Asp Gly Glu Thr Trp Glu Thr Gln 141 100 105 142 Ile Ala Ile Lys Asn Ser Arg Ala Ser Ser Val Ser Arg Val Val Asp 139 115 144 Pro Thr Val Ile Val Lys Gly Asn Lys Leu Tyr Val Leu Val Gly Ser 145 130 146 Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp 147 145 150 190 164 Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp 151 165 165 Pro Val Gln Val Thr Asn Lys Lys Gly Met His Thr Asn Gln Phe Leu 155 210 156 Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe Ser Lys Ile Phe 157 225 160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Arg Ser 158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Sphe Gly Glu Gly Arg Ser 159 245 160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu 157 255 160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Arg Ser 158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser 159 245 246 Ser Asp Met Gly Asn Strp Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser 160 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 165 290 170 170 170 170 170 170 170 170 170 170							D 110	2 .									3103
119	(2) INFORMATION FOR SEQ ID NO: 2:																
120																	
C   STRANDEDNESS: single   (D) TOPOLOGY: linear   (ii) MOLECULE TYPE: protein   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:   (2)   (3)   (3)   (2)   (2)   (3)   (3)   (2)   (2)   (3)   (																	
(i)   TOPOLOGY: linear   (ii)   MOLECULE TYPE: protein   (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 2:																	
(ii) MOLECULE TYPE: protein (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:									.e								
Met Gly Lys Thr Val Val Gly Ala Ser Arg Met Phe Trp Leu Met Phe   15																	
Met Gly Lys Thr Val Val Gly Ala Ser Arg Met Phe Trp Leu Met Phe	(	ii)	MOLE	CULE	TYP	E: p	rote	eln L. CE	O TE	NO.	ο.						
1	(XI) SEQUENCE DESCRIPTION. SEQ ID NO. 2.																
129		GTA	Lys	Thr		vaı	GTÀ	Ата	ser	10	Mec	1 110	115	ЦСи	15		
131	1		_	<b>.</b>		T a	x 1 a	LOU	Cvc		Car	Glu	Pro	Δla		Ala	
Leu Ala Pro Gly Ser Ser Arg Val Glu Leu Phe Lys Arg Gln Ser Ser  133	Phe	Val	Pro		Leu	ьeu	Ala	ьeu	Cys 25	FIO	561	GIU	110	30			
133			_	20	<i>a</i>	C = 22	1 22	17 a 1		Lon	Dho	Taye	Δrσ		Ser	Ser	
134 Lys Val Pro Phe Glu Lys Gly Gly Lys Val Thr Glu Arg Val Val His 135 50 136 Ser Phe Arg Leu Pro Ala Leu Val Asn Val Asp Gly Val Met Val Ala 137 65 70 80 138 Ile Ala Asp Ala Arg Tyr Glu Thr Ser Asn Asp Asn Ser Leu Ile Asp 139 85 90 95 140 Thr Val Ala Lys Tyr Ser Val Asp Asp Gly Glu Thr Trp Glu Thr Gln 141 100 100 105 110 142 Ile Ala Ile Lys Asn Ser Arg Ala Ser Ser Val Ser Arg Val Val Asp 135 136 157 147 Pro Thr Val Ile Val Lys Gly Asn Lys Leu Tyr Val Leu Val Gly Ser 148 130 115 120 125 144 Pro Thr Val Ile Val Lys Gly Asn Lys Leu Tyr Val Leu Val Gly Ser 145 130 135 140 146 Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp 147 145 150 150 170 170 150 Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys 180 180 181 180 190 185 190 186 Gly Gly Ala Gly Val Ala Ile Val Ala Ser Asn Gly Asn Leu Val Tyr 155 210 200 156 Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe Ser Lys Ile Phe 157 225 230 158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser 159 120 240 160 Asp Phe Gly Cys Ser Glu Pro Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser 161 162 275 280 162 Pro Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 165 290 300	Leu	Ala		GIY	ser	ser	ALG		GIU	пец	1 110	1115	45	0.2			
135	_	3	35	Dh a	<b>a</b> 1	T ***	C1 11		Twe	Val	Thr	Glu		Va1	Val	His	
136   Ser Phe Arg Leu Pro Ala Leu Val Asn Val Asp Gly Val Met Val Ala   137   65   70   70   70   70   70   70   70   7	Lys		Pro	Pne	GIU	ьуѕ		СТУ	цуз	Vai	1111	60	*** 9				
137   65	_	50	7	т о	Dwo	λla		Val	λen	Va l	Asp		Val	Met	Val	Ala	
138		Pne	Arg	Leu	PIO		Leu	Val	ASII	vul	75					80	
139	65	27-	7 an	212	λma		G1 ii	Thr	Ser	Asn		Asn	Ser	Leu	Ile	Asp	
The Val Ala Lys Tyr Ser Val Asp Asp Gly Glu The Trp Glu The Gln   100	TTE	Ата	ASP	Ата		тут	GIU	1 111	501	90					95	-	
141	m la	17.0 ]	717	T 17.0	Ψττ <b>ν</b>	Cor	Va l	Δsn	Asp		Glu	Thr	Trp	Glu	Thr	Gln	
142	Thr	Val	Ата		тут	Set	vai	дър	105				1	110			
143	T1.	A 1 -	т1.	TOO	λen	Sor	Δrα	Δla		Ser	Val	Ser	Arq	Val	Val	Asp	
144	шe	Ата		цуз	ASII	JCI	my	120	001				125			-	
145       130       135       140         146       Tyr Asn Ser Ser Arg Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp       147 145       150       155       160         148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly       160       175       160         148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly       175       175       175         150       Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys       190       175       190         152       Glu Phe Phe Pro Ala Glu Met Glu Gly Met His Thr Asn Gln Phe Leu       190       205       190         154       Gly Gly Ala Gly Val Ala Ile Val Ala Ser Asn Gly Asn Leu Val Tyr       205       205       205         155       210       215       220       220       205         156       Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe Ser Lys Ile Phe 235       240         158       Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser 240         158       Tyr Ser Glu Asp Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu 265         160       Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu 270         161       260       275         162       Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Arg Leu Val Tyr Glu Ser 285         164	Dro	mh.r	Val	т1Д	Val	Lvs	Glv		Lvs	Leu	Tvr	Val	Leu	Val	Gly	Ser	
146       Tyr Asn Ser Ser Arg       Ser Tyr Trp Thr Ser His Gly Asp Ala Arg Asp       147       148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly       160         148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly       170       175         150       Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys       180       185       190         151       180       185       190       190       190         152       Glu Phe Phe Pro Ala Glu Met Glu Gly Met His Thr Asn Gln Phe Leu       205       190       190         153       195       200       205       205       205         154       Gly Gly Ala Gly Val Ala Ile Val Ala Ile Val Ala Ser Asn Gly Asn Leu Val Tyr       220       220         155       210       215       220       235       240         155       220       235       240       235       240         156       Pro Val Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser       255       255         160       Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu       265       270         161       260       270       270         162       Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Arg Leu Val Tyr Glu Ser       285	PIO		Val	110	VUI	шуы			-1-		- 1	140			_		
147       145       150       155       160         148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly 175       150       Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys 180       175         150       Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys 190       152       Glu Phe Phe Pro Ala Glu Met Glu Gly Met His Thr Asn Gln Phe Leu 205         153       195       200       205       205         154       Gly Gly Ala Gly Val Ala Ile Val Ala Ser Asn Gly Asn Leu Val Tyr 215       210       215       220         156       210       215       220       235       240         158       Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser 245       235       240         158       Tyr Ser Glu Asp Glu Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu 265       255         160       Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu 270       265         161       11e Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Arg Leu Val Tyr Glu Ser 285         164       Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 300	mara:	130	Sor	Ser	Ara	Ser		Trp	Thr	Ser	His	Gly	Asp	Ala	Arg	Asp	
148       Trp Asp Ile Leu Leu Ala Val Gly Glu Val Thr Lys Ser Thr Ala Gly 165       165       170       175       180	_	ASII	DCI	001	5		-1	1			155	_	_			160	
149 150 150 150 150 150 150 150 150 150 150	Trn	Asp	Tle	Leu	Leu	Ala	Val	Gly	Glu	Val	Thr	Lys	Ser	Thr	Ala	Gly	
150 Gly Lys Ile Thr Ala Ser Ile Lys Trp Gly Ser Pro Val Ser Leu Lys 151					165					170					T/5		
151	Glv	Lvs	Tle	Thr	Ala	Ser	Ile	Lys	Trp	Gly	Ser	Pro	Val	Ser	Leu	Lys	
152   Glu   Phe   Phe   Pro   Ala   Glu   Met   Glu   Gly   Met   His   Thr   Asn   Gln   Phe   Leu   195   200   205     154   Gly   Gly   Ala   Gly   Val   Ala   Ile   Val   Ala   Ser   Asn   Gly   Asn   Leu   Val   Tyr   215   220     156   Pro   Val   Gln   Val   Thr   Asn   Lys   Lys   Lys   Gln   Val   Phe   Ser   Lys   Ile   Phe   230   235   240     157   225   230   235   240     158   Tyr   Ser   Glu   Asp   Glu   Gly   Lys   Thr   Trp   Lys   Phe   Gly   Glu   Gly   Arg   Ser   250   255     160   Asp   Phe   Gly   Cys   Ser   Glu   Pro   Val   Ala   Leu   Glu   Trp   Glu   Gly   Lys   Leu   265   270     162   Ile   Ile   Asn   Thr   Arg   Val   Asp   Tyr   Arg   Arg   Arg   Leu   Val   Tyr   Glu   Ser   285     164   Ser   Asp   Met   Gly   Asn   Ser   Trp   Val   Glu   Ala   Val   Gly   Thr   Leu   Ser   Arg   295   300     165   290   295   300   300   300     177   Asn   Gln   Fro   Fro				180					185					190			
153	Glu	Phe	Phe	Pro	Ala	Glu	Met	Glu	Gly	Met	His	Thr	Asn	Gln	Phe	Leu	
154 Gly Gly Ala Gly Val Ala Ile Val Ala Ser Asn Gly Asn Leu Val Tyr  155 210 215 220  156 Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe Ser Lys Ile Phe  157 225 230 230 235 240  158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser  159 245 250 255  160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu  161 260 265 270  162 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser  163 275 280  164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  165 290 295 300			195					200					205				
155	Glv	Glv	Ala	Gly	Val	Ala	Ile	Val	Ala	Ser	Asn	Gly	Asn	Leu	Val	Tyr	
156  Pro Val Gln Val Thr Asn Lys Lys Lys Gln Val Phe Ser Lys Ile Phe 157  225		210					215					220					
157 225 230 235 240  158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser  159 245 250 255  160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu  161 260 265 270  162 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser  163 275 280 285  164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  290 295 300	Pro	Val	Gln	Val	Thr	Asn	Lys	Lys	Lys	Gln	Val	Phe	Ser	Lys	Ile	Phe	
158 Tyr Ser Glu Asp Glu Gly Lys Thr Trp Lys Phe Gly Glu Gly Arg Ser 159	225					230					235					240	
159	Tvr	Ser	Glu	Asp	Glu	Gly	Lys	Thr	Trp	Lys	Phe	Gly	Glu	Gly	Arg	Ser	
160 Asp Phe Gly Cys Ser Glu Pro Val Ala Leu Glu Trp Glu Gly Lys Leu  161 260 265 270  162 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser  163 275 280 285  164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  165 290 295 300					245					250					255		
161 260 265 270  162 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser  163 275 280 285  164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  165 290 295 300	Asp	Phe	Gly	Cys	Ser	Glu	Pro	Val	Ala	Leu	Glu	Trp	Glu	Gly	Lys	Leu	
162 Ile Ile Asn Thr Arg Val Asp Tyr Arg Arg Arg Leu Val Tyr Glu Ser 163 275 280 285 164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg 165 290 295 300				260					265					270			
163 275 280 285  164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg  165 290 295 300	Ile	Ile	Asn	Thr	Arg	Val	Asp	Tyr	Arg	Arg	Arg	Leu	Val	Tyr	Glu	Ser	
164 Ser Asp Met Gly Asn Ser Trp Val Glu Ala Val Gly Thr Leu Ser Arg			275					280					285				
165 290 295 300	Ser	Asp	Met	Gly	Asn	Ser	Trp	Val	Glu	Ala	Val	Gly	Thr	Leu	Ser	Arg	
166 Val Trp Gly Pro Ser Pro Lys Ser Asn Gln Pro Gly Ser Gln Ser Ser		290					295					300					
	Val	Trp	Gly	Pro	Ser	Pro	Lys	Ser	Asn	Gln	Pro	Gly	Ser	Gln	ser	ser	

RAW SEQUENCE LISTING

DATE: 01/16/2002 TIME: 11:05:49

PATENT APPLICATION: US/09/955,909

Input Set : N:\Crf3\RULE60\09955909.raw Output Set: N:\CRF3\01162002\1955909.raw

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178	Ala	Ara	Leu	Val	Gly	Glu	Leu	Arg	Ile	Ile	Lys	Ser	Val	Leu	GIN	ser
179					105					410					413	
180	Trp	Lvs	Asn	Trp	Asp	Ser	His	Leu	Ser	Ser	Ile	Cys	Thr	Pro	Ala	Asp
181				120					425					400		
182	Pro	Ala	Ala	Ser	Ser	Ser	Glu	Arg	Gly	Cys	Gly	Pro	Ala	Val	Thr	Thr
183			425					440					447			
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/955,909
DATE: 01/16/2002
TIME: 11:05:49

Input Set : N:\Crf3\RULE60\09955909.raw
Output Set: N:\CRF3\01162002\I955909.raw

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VERIFICATION SUMMARY

DATE: 01/16/2002

PATENT APPLICATION: US/09/955,909

TIME: 11:05:50

Input Set : N:\Crf3\RULE60\09955909.raw Output Set: N:\CRF3\01162002\1955909.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]